

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/575,991
Source: IFWP
Date Processed by STIC: 04/27/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/27/2006

PATENT APPLICATION: US/10/575,991

TIME: 07:20:26

Input Set : A:\54-000711US.ST25.txt

Output Set: N:\CRF4\04272006\J575991.raw

```

3 <110> APPLICANT: The Scripps Research Institute
4     Alfonta, Lital
5     Schultz, Peter G
6     Zhang, Zhiwen
8 <120> TITLE OF INVENTION: SITE-SPECIFIC INCORPORATION OF REDOX ACTIVE AMINO ACIDS INTO
9     PROTEINS
11 <130> FILE REFERENCE: 54-000711US
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/575,991
C--> 14 <141> CURRENT FILING DATE: 2006-04-13
16 <160> NUMBER OF SEQ ID NOS: 5
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 306
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial
25 <220> FEATURE:
26 <223> OTHER INFORMATION: synthetase selected for incorporation of DHP
28 <400> SEQUENCE: 1
30 Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
31 1             5             10             15
34 Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Leu
35             20             25             30
38 Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
39             35             40             45
42 Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
43             50             55             60
46 Leu Leu Ser Asp Leu Asn Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
47 65             70             75             80
50 Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
51             85             90             95
54 Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Glu Phe Gln Leu Asp Lys
55             100            105            110
58 Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
59             115            120            125
62 Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
63             130            135            140
66 Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Asp Ile His
67 145            150            155            160
70 Tyr Leu Gly Val Asp Val Gln Val Gly Gly Met Glu Gln Arg Lys Ile
71             165            170            175
74 His Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His
75             180            185            190
78 Asn Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser

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79          195          200          205
82 Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala
83      210          215          220
86 Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro
87 225          230          235          240
90 Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys
91          245          250          255
94 Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu
95          260          265          270
98 Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys
99      275          280          285
102 Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys
103      290          295          300
106 Arg Leu
107 305
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 77
112 <212> TYPE: RNA
113 <213> ORGANISM: Artificial
115 <220> FEATURE:
116 <223> OTHER INFORMATION: mutant tRNA
118 <400> SEQUENCE: 2
119 ccggcgguag uucagcaggg cagaacggcg gacucuaaa cgcgauggcg cugguucaaa      60
121 uccggcccg cggacca      77
124 <210> SEQ ID NO: 3
125 <211> LENGTH: 918
126 <212> TYPE: DNA
127 <213> ORGANISM: Artificial
129 <220> FEATURE:
130 <223> OTHER INFORMATION: synthetase selected for incorporation of DHP
132 <400> SEQUENCE: 3
133 atggacgaat ttgaaatgat aaagagaaac acatctgaaa ttatcagcga ggaagagtta      60
135 agagaggttt taaaaaaaga tgaaaaatct gctctcatag gttttgaacc aagtggtaaa      120
137 atacatttag ggcattatct ccaaataaaa aagatgattg atttcaaaa tgctggattt      180
139 gatataatta tattgttgag cgatttaaac gcctatttaa accagaaagg agagttggat      240
141 gagattagaa aaataggaga ttataacaaa aaagtttttg aagcaatggg gttaaaggca      300
143 aaatatgttt atggaagtga attccagctt gataaggatt atacactgaa tgtctataga      360
145 ttggctttta aaactacctt aaaaagagca agaaggagta tggaacttat agcaagagag      420
147 gatgaaaatc caaaggttgc tgaagttatc tatccaataa tgcaggttta tgatattcat      480
149 tatttaggcg ttgatgttca ggttgaggag atggagcaga gaaaaatata catgttagca      540
151 agggagcttt taccaaaaaa ggttgtttgt attcacaacc ctgtcttaac gggtttgat      600
153 ggagaaggaa agatgagttc ttcaaaaggg aattttatag ctgttgatga ctctccagaa      660
155 gagattaggg ctaagataaa gaaagcatac tgcccagctg gagttgttga aggaaatcca      720
157 ataattggaga tagctaaata cttccttgaa tatcctttta ccataaaaag gccagaaaaa      780
159 tttggtggag atttgacagt taatagctat gaggagttag agagtttatt taaaaataag      840
161 gaattgcata caatggattt aaaaaatgct gtagctgaag aacttataaa gatttttagag      900
163 ccaattagaa agagatta      918
166 <210> SEQ ID NO: 4
167 <211> LENGTH: 306

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168 <212> TYPE: PRT

169 <213> ORGANISM: Methanococcus jannaschii

171 <400> SEQUENCE: 4

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173 Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
174 1          5          10          15
177 Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Tyr
178          20          25          30
181 Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
182          35          40          45
185 Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
186          50          55          60
189 Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
190 65          70          75          80
193 Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
194          85          90          95
197 Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Glu Phe Gln Leu Asp Lys
198          100         105         110
201 Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
202          115         120         125
205 Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
206          130         135         140
209 Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Asp Ile His
210 145          150         155         160
213 Tyr Leu Gly Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile
214          165         170         175
217 His Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His
218          180         185         190
221 Asn Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser
222          195         200         205
225 Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala
226          210         215         220
229 Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro
230 225         230         235         240
233 Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys
234          245         250         255
237 Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu
238          260         265         270
241 Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys
242          275         280         285
245 Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys
246          290         295         300
249 Arg Leu
250 305

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253 <210> SEQ ID NO: 5

254 <211> LENGTH: 918

255 <212> TYPE: DNA

256 <213> ORGANISM: Methanococcus jannaschii

258 <400> SEQUENCE: 5

259 atggacgaat ttgaaatgat aaagagaaac acatctgaaa ttatcagcga ggaagagtta

60

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261	agagagggttt	taaaaaaaga	tgaaaaaatct	gcttacatag	gttttgaacc	aagtggtaaa	120
263	atacatttag	ggcattatct	ccaaataaaa	aagatgattg	atttacaaaa	tgctggattt	180
265	gatataatta	tattggttgc	tgatttacac	gcctatttaa	accagaaaagg	agagttggat	240
267	gagattagaa	aaataggaga	ttataacaaa	aaagtttttg	aagcaatggg	gttaaaggca	300
269	aaatatgttt	atggaagtga	attccagctt	gataaggatt	atacactgaa	tgtctataga	360
271	ttggctttta	aaactacctt	aaaaagagca	agaaggagta	tggaacttat	agcaagagag	420
273	gatgaaaatc	caaaggttgc	tgaagttatc	tatccaataa	tgcaaggtaa	tgatattcat	480
275	tatttaggcg	ttgatgttgc	agttggaggg	atggagcaga	gaaaaataca	catgttagca	540
277	agggagcttt	tacaaaaaaa	ggttgtttgt	attcacaacc	ctgtcttaac	gggtttggat	600
279	ggagaaggaa	agatgagttc	ttcaaaaagg	aattttatag	ctgttgatga	ctctccagaa	660
281	gagattaggg	ctaagataaa	gaaagcatac	tgcccagctg	gagttgttga	aggaaatcca	720
283	ataatggaga	tagctaaata	cttccttgaa	tatcctttta	ccataaaaaag	gccagaaaaa	780
285	tttggtggag	atttgacagt	taatagctat	gaggagttag	agagtttatt	taaaaaataag	840
287	gaattgcac	caatggattt	aaaaaatgct	gtagctgaag	aacttataaa	gatttttagag	900
289	ccaattagaa	agagatta					918

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date